#15

CRF Errors Corrected by th STIC Syst m Br ch

Serial Numb r: 09/463,494A

CRF Processing Date: 3/15/02
Edited by:
Verified by: DC (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically ENTERED

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data". 1652

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

_____

***Examin r: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

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1600

RAW SEQUENCE LISTING DATE: 03/15/2002
PATENT APPLICATION: US/09/463,494A TIME: 10:41:58

Input Set : N:\Crf3\03072002\I463494A.raw
Output Set: N:\CRF3\03152002\I463494A.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Reetz, Manfred; Zonta, Albin; Schimossek, Klaus; Liebeton, Klaus; Jager, Karl-Erich
(ii) TITLE OF INVENTION: A Process for the Preparation and Identification of Novel Hydrolases Having Improved Properties
(iii) NUMBER OF SEQUENCES: 21
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Norris McLaughlin & Marcus
(B) STREET: 220 East 42nd Street, 30th Floor
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10017
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/463,494A**
C--> **(B) FILING DATE: 25-Jul-2000**
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP98/04612
(B) FILING DATE: 23-JUL-1998
(A) APPLICATION NUMBER: DE 197 31 990.4
(B) FILING DATE: 25-JUL-1997
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Briscoe, Kurt G.
(B) REGISTRATION NUMBER: 33141
(C) REFERENCE/DOCKET NUMBER: STUDIEN 268
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 808-0700
(B) TELEFAX: (212) 808-0844
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid

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Input Set : **N:\Crf3\03072002\I463494A.raw**
Output Set: **N:\CRF3\03152002\I463494A.raw**

(A) DESCRIPTION: /desc = "synthetic DNA"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
GCGCAATTAA CCCTCACTAA AGGGAACAAA 30

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
GCGTAATACG ACTCACTATA GGGCGAA 27

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017
(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC   60
CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TAT CTG CTC CCC CTC     111
                           Met Lys Lys Lys Tyr Leu Leu Pro Leu
                           -26 -25                 -20
GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG    159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                  -5
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC    207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
     1               5                  10                  15
ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT    255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                 20                  25                  30
CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC    303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
             35                  40                  45
AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG    351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
         50                  55                  60
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC    399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
     65                  70                  75
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94      GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT    447
95      Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
96       80                  85                  90                  95
97      CCC GAC CTG ATC GCT TCC GCC ATC AGC GTC GGC GCC CCG CAC AAG GGT    495
98      Pro Asp Leu Ile Ala Ser Ala Ile Ser Val Gly Ala Pro His Lys Gly
99                     100                 105                 110
100      TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC    543
101      Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
102                 115                 120                 125
103      GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC    591
104      Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
105              130                 135                 140
106      TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG    639
107      Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
108          145                 150                 155
109      GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG    687
110      Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
111      160                 165                 170                 175
112      CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC    735
113      Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
114                      180                 185                 190
115      GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC    783
116      Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
117                  195                 200                 205
118      CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG    831
119      Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
120              210                 215                 220
121      AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG    879
122      Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
123          225                 230                 235
124      GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG    927
125      Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
126      240                 245                 250                 255
127      AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC    975
128      Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
129                      260                 265                 270
130      GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG           1017
131      Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
132                  275                 280                 285
133      TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                              1049
135 (2)  INFORMATION FOR SEQ ID NO: 4:
136      (i) SEQUENCE CHARACTERISTICS:
137           (A) LENGTH: 311 amino acids
138           (B) TYPE: amino acid
139           (D) TOPOLOGY: linear
140      (ii) MOLECULE TYPE: protein
141      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
142      Met Lys Lys Lys Tyr Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
143      -26 -25                 -20                 -15
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Output Set: N:\CRF3\03152002\I463494A.raw

```
144      Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
145      -10                 -5                   1                5
146      Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
147                   10                  15                  20
148      Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
149               25                  30                  35
150      Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
151           40                  45                  50
152      Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
153       55                  60                  65                  70
154      Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
155                        75                  80                  85
156      Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
157                   90                  95                 100
158      Ile Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
159              105                 110                 115
160      Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
161          120                 125                 130
162      Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
163      135                 140                 145                 150
164      Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
165                        155                 160                 165
166      Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
167                   170                 175                 180
168      Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
169              185                 190                 195
170      Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
171          200                 205                 210
172      Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
173      215                 220                 225                 230
174      Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
175                        235                 240                 245
176      Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
177                   250                 255                 260
178      Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
179              265                 270                 275
180      Arg Leu Lys Asn Ala Ser Leu
181          280                 285
183  (2) INFORMATION FOR SEQ ID NO: 5:
184       (i) SEQUENCE CHARACTERISTICS:
185            (A) LENGTH: 1049 base pairs
186            (B) TYPE: nucleic acid
187            (C) STRANDEDNESS: unknown
188            (D) TOPOLOGY: unknown
189      (ii) MOLECULE TYPE: DNA (genomic)
190      (ix) FEATURE:
191            (A) NAME/KEY: CDS
192            (B) LOCATION:85..1017
193      (ix) FEATURE:
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Input Set : N:\Crf3\03072002\I463494A.raw
Output Set: N:\CRF3\03152002\I463494A.raw

(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC   60
CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC     111
                           Met Lys Lys Lys Ser Leu Leu Pro Leu
                           -26 -25                 -20
GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG    159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC    207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
  1               5                  10                  15
ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT    255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
              20                  25                  30
CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC    303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
          35                  40                  45
AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG    351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
      50                  55                  60
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC    399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
  65                  70                  75
GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT    447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95
CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT    495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
             100                 105                 110
TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC    543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
         115                 120                 125
GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC    591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
     130                 135                 140
TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG    639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
 145                 150                 155
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG    687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC    735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
             180                 185                 190
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC    783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
         195                 200                 205
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VERIFICATION SUMMARY DATE: 03/15/2002
PATENT APPLICATION: **US/09/463,494A** TIME: 10:41:59

Input Set : **N:\Crf3\03072002\I463494A.raw**
Output Set: **N:\CRF3\03152002\I463494A.raw**

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]